

SEQUENCE LISTING

<110> GOKHALE, Rajesh
TSUJI, Stuart
KHOSLA, Chaitan
WU, Nicholas
CANE, David

<120> METHODS TO MEDIATE POLYKETIDE SYNTHASE
MODULE EFFECTIVENESS

<130> 300622004601

<140> US 10/506,630
<141> 2002-03-04

<150> PCT/US03/06910
<151> 2002-03-04

<150> US 10/091,244
<151> 2002-03-04

<150> 60/361,758
<151> 2002-03-04

<160> 41

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Nhe site upstream of the KS at position 7570

<400> 1
gctagcgagc cgatc

15

<210> 2
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<213> Artificial Sequence

<220>
<223> Nhe site upstream of the KS at position 28710

<400> 2
gctagcgacc cgatc

15

<210> 3
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Chemically synthesized

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<221> misc feature
<223> N-terminal linker

<400> 3
Met Thr Asp Ser Glu Lys Val Ala Glu Tyr Leu Arg Arg Ala Thr Leu
1           5           10          15
Asp Leu Arg Ala Ala Arg Gln Arg Ile Arg Glu Leu Glu Ser Asp
20          25          30

<210> 4
<211> 25
<212> DNA
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<220>
<223> Primer

<400> 4
actagtaggc tgttcgccggc ctcac                                25

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
ggaaattcag gtcctctccc ccgc                                24

<210> 6
<211> 23
<212> DNA
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<220>
<223> Primer

<400> 6
ccatatggtg gtcgaccggc tcg                                23

<210> 7
<211> 24
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<220>
<223> primer

<400> 7
gaattcctac aggtcctctc cccc                                24

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

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<220>		
<223> primer		
<400> 8		22
ccatatgctg cgcgaccggc tg		
<210> 9		
<211> 25		
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<213> Artificial Sequence		
<220>		
<223> primer		
<400> 9		25
gaattctcaa tcgcccgtcga gctcc		
<210> 10		
<211> 23		
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<213> Artificial Sequence		
<220>		
<223> primer		
<400> 10		23
ccatatggtg gtcgaccggc tcg		
<210> 11		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
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<223> primer		
<400> 11		23
actagtgagg aaaccggcga ccg		
<210> 12		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 12		22
ccatatgctg cgcgaccggc tg		
<210> 13		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		

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<223> primer
<400> 13
gaattcttag ccgagctcg cgtc                                24

<210> 14
<211> 23
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<220>
<223> primer

<400> 14
ccatatggtg gtcgaccggc tcg                                23

<210> 15
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
gaattcttag aacagcctgt cccgcag                                27

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 16
ctgctcgaga ggctgttcgc ggcctca                                27

<210> 17
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 17
cccgctgagc ctacaggtcc tctcccc                                27

<210> 18
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<220>
<223> Intra-polypeptide linker

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<400> 18
Gly Gly Ala Thr Gly Ala Glu Gln Ala Ala Pro Ala Thr Thr Ala Pro
1 5 10 15
Val Asp

<210> 19
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 19
Val Gly Asp Ala Asp Gln Ala Ala Val Arg Val Val Gly Ala Ala Asp
1 5 10 15
Glu Ser

<210> 20
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 20
Val Gly Ala Ala Glu Ala Glu Gln Ala Pro Ala Leu Val Arg Glu Val
1 5 10 15
Pro Lys Asp Ala Asp
20

<210> 21
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 21
Phe Gly Ser Ala Ala Asn Arg Pro Ala Glu Ile Gly Thr Ala Ala Ala
1 5 10 15
Glu

<210> 22
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 22
Leu Gly Glu Arg Pro Ala Ala Pro Ala Pro Val Thr Arg Asp Val Ser
1 5 10 15

Asp

<210> 23
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 23
Gly Glu Thr Val Ala Gly Ala Pro Ala Thr Pro Val Thr Thr Val Ala
1 5 10 15
Asp Ala Gly

<210> 24
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 24
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser
1 5 10 15
Ala Val Gly Gln Asp
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<210> 25
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 25
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser
1 5 10 15
Val Val Gly Gln Asp
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<210> 26
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 26
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser
1 5 10 15
Ala Gly Gln Asp
20

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<210> 27
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 27
Val Thr Asp Ser Glu Lys Val Ala Glu Tyr Leu Arg Arg Ala Thr Leu
1 5 10 15
Asp Leu Arg Ala Ala Arg Gln Arg Ile Arg Glu Leu Glu Ser
20 25 30

<210> 28
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 28
Met Ser Gly Asp Asn Gly Met Thr Glu Glu Lys Leu Arg Arg Tyr Leu
1 5 10 15
Lys Arg Thr Val Thr Glu Leu Asp Ser Val Thr Ala Arg Leu Arg Glu
20 25 30
Val Glu His Arg Ala Gly
35

<210> 29
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 29
Met Ser Ala Pro Asn Glu Gln Ile Val Asp Ala Leu Arg Ala Ser Leu
1 5 10 15
Lys Glu Asn Val Arg Leu Gln Gln Glu Asn Ser Ala Leu Ala Ala Ala
20 25 30
Ala Ala

<210> 30
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 30
Val Ser Ala Ser Tyr Glu Lys Val Val Glu Ala Leu Arg Lys Ser Leu
1 5 10 15

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Glu Glu Val Gly Thr Leu Lys Lys Arg Asn Arg Gln Leu Ala Asp Ala
20 25 30
Ala Gly

<210> 31
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 31
Val Ala Asp Glu Gly Gln Leu Arg Asp Tyr Leu Lys Arg Ala Ile Ala
1 5 10 15
Asp Ala Arg Asp Ala Arg Thr Arg Leu Arg Glu Val Glu Glu Gln Ala
20 25 30
Arg

<210> 32
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 32
Met Ala Thr Asp Glu Lys Leu Leu Lys Tyr Leu Lys Arg Val Thr Ala
1 5 10 15
Glu Leu His Ser Leu Arg Lys Gln Gly Ala Arg His Ala Asp
20 25 30

<210> 33
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 33
Met Arg Glu Asp Gln Leu Leu Asp Ala Leu Arg Lys Ser Val Lys Glu
1 5 10 15
Asn Ala Arg Leu Arg Lys Ala Asn Thr Ser Leu Arg Ala Ala Met Asp
20 25 30

<210> 34
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 34

Met Pro Glu Gln Asp Lys Val Val Glu Tyr Leu Arg Trp Ala Thr Ala
1 5 10 15
Glu Leu His Thr Thr Arg Ala Lys Leu Glu Ala Leu Ala Ala Ala Asn
20 25 30
Thr

<210> 35
<211> 388
<212> PRT
<213> Artificial Sequence

<220>
<223> Alignment of the EryA SU

<400> 35
Val Val Phe Val Phe Pro Gly Gln Gly Ala Gln Trp Ala Gly Met Ala
1 5 10 15
Gly Glu Leu Ile Gly Glu Ser Arg Val Phe Ala Ala Ala Met Asp Ala
20 25 30
Cys Ala Arg Ala Phe Glu Pro Val Thr Asp Trp Thr Leu Ala Gln Val
35 40 45
Leu Asp Ser Pro Glu Gln Ser Arg Arg Val Glu Val Val Gln Pro Ala
50 55 60
Leu Phe Ala Val Gln Thr Ser Leu Ala Ala Leu Trp Arg Ser Phe Gly
65 70 75 80
Val Thr Pro Asp Ala Val Val Gly His Ser Ile Gly Glu Leu Ala Ala
85 90 95
Ala His Val Cys Gly Ala Ala Gly Ala Ala Asp Ala Ala Arg Ala Ala
100 105 110
Ala Leu Trp Ser Arg Glu Met Ile Pro Ile Val Gly Asn Gly Asp Met
115 120 125
Met Ala Val Ala Leu Ser Ala Asp Glu Ile Glu Pro Arg Ile Ala Arg
130 135 140
Trp Asp Asp Val Val Leu Ala Gly Val Asn Gly Pro Arg Ser Val Leu
145 150 155 160
Leu Thr Gly Ser Pro Glu Pro Val Ala Arg Arg Val Gln Glu Leu Ser
165 170 175
Ala Glu Gly Val Arg Ala Gln Val Ile Asn Val Ser Met Ala Ala His
180 185 190
Ser Ala Gln Val Asp Asp Ile Ala Glu Gly Met Arg Ser Ala Leu Ala
195 200 205
Trp Phe Ala Pro Gly Gly Ser Glu Val Pro Phe Tyr Ala Ser Leu Thr
210 215 220
Gly Gly Ala Val Asp Thr Arg Glu Leu Val Ala Asp Tyr Trp Arg Arg
225 230 235 240
Ser Phe Arg Leu Pro Val Arg Phe Asp Glu Ala Ile Arg Ser Ala Leu
245 250 255
Glu Val Gly Pro Gly Thr Phe Val Glu Ala Ser Pro His Pro Val Ile
260 265 270
Ala Ala Ala Leu Gln Gln Thr Leu Asp Ala Glu Gly Ser Ser Ala Ala
275 280 . 285
Val Val Pro Thr Leu Gln Arg Gly Gln Gly Gly Met Arg Arg Phe Leu
290 295 300
Leu Ala Ala Ala Gln Ala Phe Thr Gly Gly Val Ala Val Asp Trp Thr
305 310 315 320
Ala Ala Tyr Asp Asp Val Gly Pro Asn Pro Ala Leu Gly Arg Glu Ala
325 330 335
Asp Ala Glu Ala Thr Phe Arg Glu Leu Gly Leu Asp Ser Val Leu Ala
340 345 350
Ala Gln Ile Arg Ala Lys Val Ser Ala Ala Ile Gly Arg Glu Val Asn
355 360 365

Ile Ala Leu Leu Tyr Asp His Pro Thr Pro Arg Ala Leu Ala Glu Ala
 370 375 380
 Leu Ala Ala Gly
 385

<210> 36
 <211> 1397
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Alignment of the EryA SU

<400> 36
 Ala Ala Pro Gly Glu Pro Val Ala Val Val Ala Met Ala Cys Arg Leu
 1 5 10 15
 Pro Gly Gly Val Ser Thr Pro Glu Glu Phe Trp Glu Leu Leu Ser Glu
 20 25 30
 Gly Arg Asp Ala Val Ala Gly Leu Pro Thr Asp Arg Gly Trp Asp Leu
 35 40 45
 Asp Ser Leu Phe His Pro Asp Pro Thr Arg Ser Gly Thr Ala His Gln
 50 55 60
 Arg Gly Gly Phe Leu Thr Glu Ala Thr Ala Phe Asp Pro Ala Phe
 65 70 75 80
 Phe Gly Met Ser Pro Arg Glu Ala Leu Ala Val Asp Pro Gln Gln Arg
 85 90 95
 Leu Met Leu Glu Leu Ser Trp Glu Val Leu Glu Arg Ala Gly Ile Pro
 100 105 110
 Pro Thr Ser Ile Gln Ala Ser Pro Thr Gly Val Phe Val Gly Leu Ile
 115 120 125
 Pro Gln Glu Tyr Gly Pro Arg Leu Ala Glu Gly Gly Glu Gly Val Glu
 130 135 140
 Gly Tyr Leu Met Thr Gly Thr Thr Ser Val Ala Ser Gly Arg Ile
 145 150 155 160
 Ala Tyr Thr Leu Gly Leu Glu Gly Pro Ala Ile Ser Val Asp Thr Ala
 165 170 175
 Cys Ser Ser Ser Leu Val Ala Val His Leu Ala Cys Gln Ser Leu Arg
 180 185 190
 Arg Gly Glu Ser Ser Ile Ala Met Ala Gly Gly Val Thr Val Met Pro
 195 200 205
 Thr Pro Gly Met Leu Val Asp Phe Ser Arg Met Asn Ser Leu Ala Pro
 210 215 220
 Asp Gly Arg Cys Lys Ala Phe Ser Ala Gly Ala Asn Gly Phe Gly Met
 225 230 235 240
 Ala Glu Gly Ala Gly Met Leu Leu Ile Glu Arg Leu Ser Asp Ala Arg
 245 250 255
 Arg Asn Gly His Pro Val Leu Ala Val Leu Arg Gly Thr Ala Val Asn
 260 265 270
 Ser Asp Gly Ala Ser Asn Gly Leu Ser Ala Pro Asn Gly Arg Ala Gln
 275 280 285
 Val Arg Val Ile Gln Gln Ala Leu Ala Glu Ser Gly Leu Gly Pro Ala
 290 295 300
 Asp Ile Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp
 305 310 315 320
 Pro Ile Glu Ala Arg Ala Leu Phe Glu Ala Tyr Gly Arg Asp Arg Glu
 325 330 335
 Gln Pro Leu His Leu Gly Ser Val Lys Ser Asn Leu Gly His Thr Gln
 340 345 350
 Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met Arg
 355 360 365
 Ala Gly Thr Leu Pro Arg Thr Leu His Ala Ser Glu Arg Ser Lys Glu

370	375	380
Ile Asp Trp Ser Ser Gly Ala Ile Ser Leu Ile	Asp Glu Pro Glu Pro	
385	390	395 400
Trp Pro Ala Gly Ala Arg Pro Arg Arg Ala	Gly Val Ser Ser Phe Gly	
405	410	415
Ile Ser Gly Thr Asn Ala His Ala Ile Ile	Glu Glu Ala Pro Gln Val	
420	425	430
Val Glu Gly Glu Arg Val Glu Ala Gly Asp Val Val	Ala Pro Trp Val	
435	440	445
Leu Ser Ala Ser Ser Ala Glu Gly Leu Arg Ala	Gln Ala Ala Arg Leu	
450	455	460
Ala Ala His Leu Arg Glu His Pro Gly Gln Asp	Pro Arg Asp Ile Ala	
465	470	475 480
Tyr Ser Leu Ala Thr Gly Arg Ala Ala	Leu Pro His Arg Ala Ala Phe	
485	490	495
Ala Pro Val Asp Glu Ser Ala Ala	Leu Arg Val Leu Asp Gly Leu Ala	
500	505	510
Thr Gly Asn Ala Asp Gly Ala Ala Val Gly Thr	Ser Arg Ala Gln Gln	
515	520	525
Arg Ala Val Phe Val Trp Ala Ala Val Asp Asp	Thr Ser Pro Ala Ala	
530	535	540
Leu Arg Glu Ala Asp Ala Leu Glu Pro His	Leu Asp Arg Glu Val Ile	
545	550	555 560
Pro Phe Leu Arg Ala Glu Ala Ala Arg	Arg Glu Gln Asp Ala Ala Leu	
565	570	575
Ser Thr Glu Asp Val Val Met Ala Val Met Val	Ser Met Arg Ala His	
580	585	590
Val Glu Ala Ile Gln Ile Cys Ala Ala	Leu Ser Leu Asp Asp Ala Ala	
595	600	605
Arg Val Val Ala Leu Arg Ser Arg Val Ile Ala	Thr Met Pro Gly Asn	
610	615	620
Lys Gly Ala Ser Ile Ala Ala Pro Ala Gly	Glu Val Arg Ala Arg Ile	
625	630	635 640
Gly Asp Arg Val Glu Ile Ala Gly Arg Ser	Val Val Val Ala Asp Ser	
645	650	655
Asp Glu Leu Asp Arg Leu Val Ala Ser Cys	Thr Thr Glu Cys Ile Arg	
660	665	670
Ala Lys Arg Leu Ala Asp Tyr Ser Ser Ser His	Val Glu Thr Ile Arg	
675	680	685
Asp Ala Leu His Ala Glu Leu Gly Glu Asp Phe	His Pro Leu Pro Gly	
690	695	700
Phe Val Pro Phe Phe Thr Val Thr Gly Arg	Trp Thr Gln Pro Asp Glu	
705	710	715 720
Leu Asp Ala Gly Tyr Arg Asn Ile Arg	Thr Arg Ala Asp Val Arg Ala	
725	730	735
Leu Ala Glu Gln Tyr Arg Thr Leu Val Ala Ile	Leu Thr Ala Ala Ile	
740	745	750
Glu Glu Ile Gly Asp Gly Ser Gly Ala Asp Leu	Ser Ala Ile His Ser	
755	760	765
Arg Gly Asp Gly Ser Leu Ala Asp Phe Gly	Glu Ala Leu Ser Arg Phe	
770	775	780
Ala Ala Ala Val Asp Trp Glu Ser Val His	Leu Gly Thr Gly Ala Arg	
785	790	795 800
Arg Val Pro Leu Pro Thr Tyr Pro Phe Gln	Arg Glu Arg Val Trp Leu	
805	810	815
Glu Pro Lys Pro Val Ala Arg Arg Ser Thr	Glu Val Asp Glu Val Ser	
820	825	830
Ala Leu Arg Tyr Arg Ile Glu Trp Arg Pro	Thr Gly Ala Gly Glu Pro	
835	840	845
Ala Arg Leu Asp Gly Thr Trp Leu Val Ala Lys	Tyr Ala Gly Thr Ala	
850	855	860
Asp Glu Thr Ser Thr Ala Ala Arg Glu Ala	Leu Glu Ser Ala Gly Ala	

865	870	875	880
Arg Val Arg Glu Leu Val Val Asp Ala Arg Cys Gly Arg Asp Glu Leu			
885	890	895	
Ala Glu Arg Leu Arg Ser Val Gly Glu Val Ala Gly Val Leu Ser Leu			
900	905	910	
Leu Ala Val Asp Glu Ala Glu Pro Glu Glu Ala Pro Leu Ala Leu Ala			
915	920	925	
Ser Leu Ala Asp Thr Leu Ser Leu Val Gln Ala Met Val Ser Ala Glu			
930	935	940	
Leu Gly Cys Pro Leu Trp Thr Val Thr Glu Ser Ala Val Ala Thr Gly			
945	950	955	960
Pro Phe Glu Arg Val Arg Asn Ala Ala His Gly Ala Leu Trp Gly Val			
965	970	975	
Gly Arg Val Ile Ala Leu Glu Asn Pro Ala Val Trp Gly Gly Leu Val			
980	985	990	
Asp Val Pro Ala Gly Ser Val Ala Glu Leu Ala Arg His Leu Ala Ala			
995	1000	1005	
Val Val Ser Gly Gly Ala Gly Glu Asp Gln Leu Ala Leu Arg Ala Asp			
1010	1015	1020	
Gly Val Tyr Gly Arg Arg Trp Val Arg Ala Ala Pro Ala Thr Asp			
1025	1030	1035	1040
Asp Glu Trp Lys Pro Thr Gly Thr Val Leu Val Thr Gly Gly Thr Gly			
1045	1050	1055	
Gly Val Gly Gly Gln Ile Ala Arg Trp Ile Ala Arg Pro Gly Ala Pro			
1060	1065	1070	
His Leu Leu Leu Val Ser Arg Ser Gly Pro Asp Ala Asp Gly Ala Gly			
1075	1080	1085	
Glu Leu Val Ala Glu Leu Glu Ala Leu Gly Ala Arg Thr Thr Val Ala			
1090	1095	1100	
Ala Cys Asp Val Ile Asp Arg Glu Ser Val Arg Glu Leu Leu Gly Gly			
1105	1110	1115	1120
Ile Gly Asp Asp Val Pro Leu Ser Ala Val Phe His Ala Ala Ala Thr			
1125	1130	1135	
Leu Asp Asp Gly Thr Val Asp Thr Leu Thr Gly Glu Arg Ile Glu Arg			
1140	1145	1150	
Ala Ser Arg Ala Lys Val Leu Gly Ala Arg Asn Leu His Glu Leu Thr			
1155	1160	1165	
Arg Glu Leu Asp Leu Thr Ala His Val Leu Phe Ser Ser Phe Ala Ser			
1170	1175	1180	
Ala Phe Gly Ala Pro Gly Leu Gly Gly Tyr Ala Pro Gly Asn Ala Tyr			
1185	1190	1195	1200
Leu Asp Gly Leu Ala Gln Gln Arg Arg Ser Asp Gly Leu Pro Ala Thr			
1205	1210	1215	
Ala Val Ala Trp Gly Thr Trp Ala Gly Ser Gly Met Ala Glu Gly Ala			
1220	1225	1230	
Val Ala Asp Arg Phe Arg Arg His Gly Val Ile Glu Met Pro Pro Glu			
1235	1240	1245	
Thr Ala Cys Arg Ala Leu Gln Asn Ala Leu Asp Arg Ala Glu Val Cys			
1250	1255	1260	
Pro Ile Val Ile Asp Val Arg Trp Asp Arg Phe Leu Leu Ala Tyr Thr			
1265	1270	1275	1280
Ala Gln Arg Pro Thr Arg Leu Phe Asp Glu Ile Asp Asp Ala Arg Arg			
1285	1290	1295	
Ala Ala Pro Gln Ala Pro Ala Glu Pro Arg Val Gly Ala Leu Ala Ser			
1300	1305	1310	
Leu Pro Ala Pro Glu Arg Glu Glu Ala Leu Phe Glu Leu Val Arg Ser			
1315	1320	1325	
His Ala Ala Ala Val Leu Gly His Ala Ser Ala Glu Arg Val Pro Ala			
1330	1335	1340	
Asp Gln Ala Ala Glu Val Leu Ser Leu Glu Asn Arg Leu Gly Ala Ala			
1345	1350	1355	1360
Thr Val Arg Leu Pro Thr Thr Val Phe Asp Asp Val Arg Thr Leu			

1365	1370	1375
Ala His Leu Ala Ala Glu Leu Gly Gly Ala Thr Gly Ala Glu Gln Ala		
1380	1385	1390
Ala Pro Ala Thr Thr		
1395		

<210> 37
<211> 1114
<212> PRT
<213> Artificial Sequence

<220>
<223> Alignment of the EryA SU

<400> 37			
Ala Pro Val Asp Glu Ile Ile Gly Met Ala Leu Glu Val Asp Ser Glu			
1	5	10	15
Arg Leu Glu Leu Ile Thr Ser Gly Arg Asp Ser Ala Ala Glu Val Asp			
20	25	30	
Val Pro Asp Glu Leu Met Ala Ser Asp Ala Ala Gly Thr Arg Ala His			
35	40	45	
Asn Phe Met Ala Gly Gly Asp Ala Ala Ile Ser Leu Met Gln Ala Thr			
50	55	60	
Thr Ala Leu Ser Ile Pro Glu Thr Arg Gly Ser Asp Val Met Ser His			
65	70	75	80
Gln Gly Ala Thr Gly Arg Pro Arg Pro Glu Asp Gly Val Asp Leu Leu			
85	90	95	
Thr Asn Thr Ala Ser Ala Ile Ala Val Leu Leu Ala Leu Thr Ser Val			
100	105	110	
Ala Leu Thr Cys Gly Ser Asp Gly Asp Gln Gly Leu Val Ala Val Ser			
115	120	125	
Ala Gly Glu Val Phe Thr Glu Ser Arg Gln Gly Ala Ser Pro Cys Pro			
130	135	140	
Ser Asp Glu Asp Gly Leu Gly Ser Ala Phe Val Val Gln Arg Asp Arg			
145	150	155	160
Glu Arg Arg Gly Val Val Ala Ser Val Gln Ser Ser Val Ala Gln Arg			
165	170	175	
Arg Trp Ala Arg Ala Ile Thr Gly Ala Val Ala Val Arg Val Ala Ser			
180	185	190	
Leu Ala Thr Lys Ser Gly Ser Ser Gly Val Leu Leu Ser Ile Ala Val			
195	200	205	
Ala Ile Val Ile Gly Leu Glu Arg Val Val Pro Met Cys Arg Gly Arg			
210	215	220	
Ser Gly Leu Ile Asp Ser Ser Glu Ile Glu Leu Ala Asp Gly Val Arg			
225	230	235	240
Glu Ser Pro Ala Ala Asp Gly Val Gly Ala Val Val Ile Ala Pro Glu			
245	250	255	
Pro Glu Pro Val Pro Gln Pro Arg Arg Met Leu Pro Ala Thr Gly Val			
260	265	270	
Val Val Val Leu Ala Arg Thr Gly Ala Ala Leu Arg Gly Arg Leu Ala			
275	280	285	
Asp His Leu Ala Ala His Pro Gly Ile Ala Pro Ala Asp Val Ser Trp			
290	295	300	
Thr Met Arg Ala Gln His Phe Glu Glu Ala Val Leu Ala Ala Asp Thr			
305	310	315	320
Ala Glu Ala Val His Arg Arg Ala Val Asp Ala Val Val Pro Gly Val			
325	330	335	
Val Thr Gly Ser Ala Ser Asp Gly Gly Ser Val Phe Val Ala Glu Ala			
340	345	350	
Arg Glu Pro Val Pro Glu Ser Ile Ala Glu Asp Ala Val Leu Ser Glu			
355	360	365	

Val Ala Gly Arg Ser Val Ser Glu Val Leu Glu Pro Arg Pro Asp Ala
 370 375 380
 Pro Ser Leu Glu Asp Val Val Leu Ala Val Met Val Arg Leu Arg Ala
 385 390 395 400
 Cys Ala Val Ser Ile Gln Ile Val Ala Ala Leu Ser Leu Glu Asp Gly
 405 410 415
 Met Arg Val Val Ala Arg Arg Ser Arg Ala Val Arg Ala Val Ala Gly
 420 425 430
 Arg Gly Ser Leu Ser Val Arg Gly Gly Arg Ser Asp Val Glu Lys Leu
 435 440 445
 Leu Ala Asp Asp Ser Trp Thr Gly Arg Leu Glu Val Ala Gly Asp Ala
 450 455 460
 Val Val Val Ala Asp Ala Gln Ala Ala Arg Glu Phe Leu Glu Tyr Cys
 465 470 475 480
 Glu Gly Val Gly Ile Arg Ala Arg Ala Ile Pro Asp Tyr Ser Thr Ala
 485 490 495
 His Val Glu Pro Val Arg Asp Glu Leu Val Gln Ala Leu Ala Gly Ile
 500 505 510
 Thr Pro Arg Arg Ala Glu Val Pro Phe Phe Thr Leu Thr Gly Asp Phe
 515 520 525
 Leu Asp Gly Thr Glu Leu Asp Ala Gly Tyr Arg Asn Ile His Pro Glu
 530 535 540
 His Ser Val Gln Ala Leu Thr Asp Gln Tyr Ala Thr Ile Val Pro Val
 545 550 555 560
 Leu Ala Ser Ser Val Gln Glu Thr Leu Asp Asp Ala Glu Ser Asp Ala
 565 570 575
 Ala Val Leu Gly Thr Glu Asp Ala Gly Asp Ala Asp Arg Phe Leu Thr
 580 585 590
 Ala Leu Ala Asp His Thr Arg Ala Val Asp Trp Glu Ala Val Leu Gly
 595 600 605
 Arg Ala Gly Leu Val Asp Gly Gln Gly Lys Phe Leu Leu Pro Asp Arg
 610 615 620
 Thr Thr Pro Arg Glu Leu Asp Gly Trp Phe Arg Val Asp Thr Glu Val
 625 630 635 640
 Pro Arg Ser Glu Pro Ala Ala Leu Arg Gly Arg Trp Val Val Val Pro
 645 650 655
 Glu Gly His Glu Glu Asp Gly Trp Thr Val Glu Val Arg Ser Ala Leu
 660 665 670
 Ala Glu Ala Ala Glu Pro Glu Val Thr Arg Gly Val Gly Leu Val
 675 680 685
 Gly Asp Cys Ala Gly Val Leu Leu Ala Leu Glu Gly Asp Gly Ala Val
 690 695 700
 Gln Thr Leu Val Val Arg Glu Leu Asp Ala Glu Gly Ile Asp Ala Pro
 705 710 715 720
 Leu Trp Thr Val Phe Gly Asp Ala Gly Ser Pro Val Ala Arg Pro Asp
 725 730 735
 Gln Ala Lys Leu Trp Leu Gly Gln Val Ala Ser Leu Arg Gly Pro Arg
 740 745 750
 Trp Thr Gly Leu Val Leu Pro His Met Pro Asp Pro Glu Leu Arg Gly
 755 760 765
 Arg Leu Thr Val Leu Ala Gly Ser Glu Asp Gln Val Val Ala Asp Ala
 770 775 780
 Val Arg Ala Arg Leu Ser Pro Ala His Val Thr Ala Thr Ser Glu Tyr
 785 790 795 800
 Ala Val Gly Ile Val Gly Thr Ala Gly Leu Ala Glu Val Ala Trp Ala
 805 810 815
 Gly Arg Ala Glu His Ala Val Ser Arg Arg Gly Pro Asp Thr Glu Gly
 820 825 830
 Val Gly Asp Thr Ala Glu Leu Thr Asp Leu Ala Arg Val Ser Val His
 835 840 845
 Cys Val Ser Ser Arg Glu Pro Val Arg Glu Ile Val His Gly Leu Ile
 850 855 860

Glu Gln Gly Asp Val Val Arg Gly Val Val Ala Ala Gly Leu Pro Gln
 865 870 875 880
 Gln Val Ala Ile Asn Asp Met Asp Glu Ala Ala Phe Asp Glu Val Val
 885 890 895
 Ala Ala Ala Gly Gly Ala Val His Asp Leu Cys Ser Asp Ala Glu Leu
 900 905 910
 His Leu Ile Phe Gly Gly Val Trp Gly Ser Ala Arg Gln Gly Ala Ala
 915 920 925
 Ala Gly Asn Ala Phe Asp Ala Phe Arg His Arg Gly Arg Leu Pro Ala
 930 935 940
 Thr Ser Val Ala Gly Leu Ala Gly Gly Met Thr Gly Asp Glu Glu Ala
 945 950 955 960
 Val Ser Phe Leu Arg Glu Arg Val Arg Ala Met Pro Val Pro Arg Leu
 965 970 975
 Ala Ala Leu Asp Arg Val Ala Ser Gly Glu Thr Ala Val Val Val Thr
 980 985 990
 Asp Val Asp Trp Pro Ala Phe Ala Glu Ser Tyr Thr Ala Arg Pro Arg
 995 1000 1005
 Pro Leu Leu Asp Arg Ile Val Thr Thr Ala Pro Ser Glu Arg Ala Gly
 1010 1015 1020
 Glu Pro Glu Thr Glu Ser Leu Arg Asp Arg Leu Gly Leu Pro Arg Ala
 1025 1030 1035 1040
 Glu Arg Thr Ala Glu Val Arg Leu Val Arg Thr Ser Thr Thr Val Leu
 1045 1050 1055
 His Asp Asp Pro Lys Ala Val Arg Ala Thr Thr Pro Lys Glu Phe Leu
 1060 1065 1070
 Ala Val Arg Asn Leu Leu Asn Ala Ala Thr Leu Arg Leu Pro Ser Thr
 1075 1080 1085
 Leu Val Phe Asp Asn Ala Ser Ala Val Gly Phe Leu Asp Ala Glu Gly
 1090 1095 1100
 Thr Glu Val Arg Gly Glu Ala Pro Ser Ala
 1105 1110

<210> 38
 <211> 1128
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Alignment of the EryA SU

<400> 38
 Glu Leu Glu Ser Asp Ile Ile Ser Met Ala Leu Gly Val Asn Thr Gln
 1 5 10 15
 Arg Ile Glu Leu Leu Arg Glu Gly Gly Glu Thr Leu Ser Gly Phe Thr
 20 25 30
 Asp Leu Ala Arg Leu His His Pro Asp Pro Asp Asn Pro Gly Thr Ser
 35 40 45
 Tyr Val Asp Lys Gly Phe Leu Asp Asp Ala Gly Ala Glu Val Ser Ala
 50 55 60
 Met Leu Ile Thr Ser Leu Val Asn Ile Asp His Ser Arg Gly Thr Ala
 65 70 75 80
 Leu Val Ala Lys Phe Gly Gly Glu Asp Thr Ala Ala Ala Glu Asp Val
 85 90 95
 Glu Ser Val Thr Val Ala Pro Ala Ala Ile Ser Thr Met Leu Ser Ile
 100 105 110
 Ser Ser Val Ala Leu Ile Val Glu Ser Lys Gly Glu Ser Ser Met Val
 115 120 125
 Val Ala Ala Ala Thr Gly Val Phe Val Asp Ser Arg Gln Arg Ala Ala
 130 135 140
 Ala Ser Ala Gly Ala Gly Asp Gly Phe Ser Val Thr Leu Val Leu Glu

145	150	155	160
Arg Glu Arg Asn His	Glu Ala Val Val	Arg Ser Ile Gln Ser Ser Pro	
165	170	175	
Ala Arg Arg Gln Leu Glu Ser Cys	Leu Glu Pro Gly Val Asp Ala Ala		
180	185	190	
Ile Ala Asn Leu Asp Thr Arg Asp Asp Ala Asp Arg	Leu Trp Leu Ser		
195	200	205	
Ile Thr Val Thr Leu Val Val Ala Leu Arg Asn	Glu Leu Ala Thr His		
210	215	220	
Val Glu Pro Thr Pro His Val Asp Ser Ser	Gly Val Ala Leu Leu Ala		
225	230	235	240
Gly Asn Gln Pro Arg Arg Gly Glu Arg Thr Arg Ala Ile	Val Val Glu		
245	250	255	
Ala Glu Arg Glu His Arg Glu Thr Thr Ala His Asp Gly Arg Pro Val			
260	265	270	
Leu Val Val Ala Arg Thr Thr Ala Ala Leu Arg Ala	Gln Ile Ala Glu		
275	280	285	
Leu Leu Glu Arg Pro Asp Ala Asp Leu Ala Gly Val Gly Leu Gly Leu			
290	295	300	
Thr Thr Ala Arg His Glu His Ala Val Val Ala Ser Thr Arg Glu Glu			
305	310	315	320
Ala Val Arg Gly Arg Glu Ile Ala Ala Ala Thr Ala Asp Ala Val Val			
325	330	335	
Glu Gly Val Thr Glu Val Asp Gly Arg Asn Val Val Phe Leu Ser Ala			
340	345	350	
Gly Ala Glu Ser Ser Ser Pro Gly Lys Ile Arg Ala Asp Glu Ser Met			
355	360	365	
Ala Pro Met Gln Asp Trp Lys Val Ser Asp Val Leu Arg Gln Ala Pro			
370	375	380	
Gly Ala Pro Gly Leu Asp Asp Val Val Leu Val Met Val Glu Leu Arg			
385	390	395	400
Ser Tyr Val Glu Ala Val Gln Ile His Ala Ala Leu Thr Leu Glu Asp			
405	410	415	
Ala Ala Lys Ile Val Val Gly Arg Ser Arg Ile Met Arg Ser Leu Ser			
420	425	430	
Gly Glu Gly Gly Ala Ala Val Ala Leu Gly Glu Ala Ala Val Arg Glu			
435	440	445	
Arg Leu Arg Pro Trp Gln Asp Arg Leu Ser Val Ala Gly Arg Ser Val			
450	455	460	
Val Val Ser Glu Pro Gly Ala Leu Arg Ala Phe Ser Glu Asp Cys Ala			
465	470	475	480
Ala Glu Gly Ile Arg Val Arg Asp Ile Asp Asp Tyr Ser Ser Pro Gln			
485	490	495	
Ile Glu Arg Val Arg Glu Glu Leu Leu Glu Thr Thr Gly Asp Ile Ala			
500	505	510	
Pro Arg Pro Ala Arg Val Pro Phe His Thr Val Glu Ser Arg Ser Met			
515	520	525	
Asp Gly Thr Glu Leu Asp Ala Arg Tyr Arg Asn Ile Glu Thr Arg Ala			
530	535	540	
Asp Val Thr Arg Leu Ala Glu Ser Tyr Asp Ala Ile Val Pro Val Val			
545	550	555	560
Val Gln Ala Val Glu Glu Gln Val Glu Glu Ala Asp Gly Ala Glu Asp			
565	570	575	
Ala Val Val Val Gly Ser His Asp Gly Gly Asp Leu Ser Ala Phe Leu			
580	585	590	
Arg Ser Met Ala Thr His Val Ser Asp Ile Arg Trp Asp Val Ala Leu			
595	600	605	
Pro Gly Ala Ala Pro Phe Ala Thr Gln Arg Lys Tyr Leu Gln Pro Ala			
610	615	620	
Ala Pro Ala Ala Ala Ser Glu Leu Ala Arg Val Ser Thr Pro Ile Glu			
625	630	635	640
Lys Pro Glu Ser Gly Asn Leu Asp Gly Asp Trp Val Val Thr Pro Leu			

645	650	655
Ile Ser Pro Glu Trp Thr Glu Met Leu Cys Glu Ala Ile Asn Ala Asn		
660	665	670
Gly Arg Ala Leu Arg Cys Glu Val Asp Thr Ser Ala Ser Arg Thr Glu		
675	680	685
Met Ala Gln Ala Val Ala Gln Ala Gly Thr Gly Phe Arg Gly Leu Leu		
690	695	700
Leu Ser Ser Asp Glu Ser Ala Cys Arg Pro Gly Val Pro Ala Gly Ala		
705	710	715
Val Gly Leu Leu Thr Val Gln Ala Leu Gly Asp Ala Gly Val Asp Ala		
725	730	735
Pro Val Trp Cys Leu Gln Gly Arg Thr Pro Ala Asp Asp Asp Leu Ala		
740	745	750
Arg Pro Ala Gln Thr Thr Ala His Phe Ala Gln Val Ala Gly Leu Leu		
755	760	765
Pro Gly Arg Trp Gly Gly Val Val Leu Pro Glu Ser Val Asp Asp Ala		
770	775	780
Ala Leu Arg Leu Leu Val Val Leu Arg Gly Gly Arg Ala Glu Asp		
785	790	795
His Leu Val Asp Gly Arg Leu His Gly Arg Val Val Arg Ala Ser Leu		
805	810	815
Pro Gln Ser Gly Ser Arg Ser Trp Thr His Val Val Ala Ala Ser Pro		
820	825	830
Val Asp Gln Ile Val Trp Ala Asp Arg Ala Glu Arg Val Ala Gly Ala		
835	840	845
Cys Pro Gly Asp Asp Leu Ala Ala Val Glu Glu Ala Ala Ser Ala Val		
850	855	860
Val Cys Gln Ala Ala Leu Arg Glu Ala Leu Gly Asp Glu Pro Val		
865	870	875
Thr Ala Leu Val Ala Gly Thr Leu Thr Asn Phe Gly Ser Ile Ser Glu		
885	890	895
Val Ala Pro Glu Glu Phe Ala Glu Thr Ile Ala Ala Thr Ala Leu Leu		
900	905	910
Ala Val Asp Val Leu Gly Asp Arg Ala Val Glu Arg His Val Tyr Cys		
915	920	925
Val Gly Ile Trp Gly Gly Ala Gly Met Ala Ala Ala Gly Ser Ala		
930	935	940
Tyr Asp Ala Leu Glu His His Ala Arg Arg Ser Cys Thr Ser Val Ala		
945	950	955
Thr Pro Leu Pro Gly Gly Ala Val Asp Asp Gly Tyr Leu Arg Glu Arg		
965	970	975
Leu Arg Ser Leu Ser Ala Asp Arg Met Arg Thr Trp Glu Arg Val Ala		
980	985	990
Ala Gly Pro Val Ser Val Ala Val Ala Asp Val Asp Trp Pro Val Leu		
995	1000	1005
Ser Glu Gly Phe Ala Thr Arg Pro Thr Ala Leu Phe Ala Glu Leu Ala		
1010	1015	1020
Gly Arg Gly Gly Gln Ala Glu Ala Glu Pro Asp Ser Gly Pro Thr Gly		
1025	1030	1035
Glu Pro Ala Gln Arg Leu Gly Leu Ser Pro Asp Glu Gln Gln Glu Asn		
1045	1050	1055
Leu Glu Leu Val Ala Asn Ala Val Glu Val Leu His Glu Ser Ala Ala		
1060	1065	1070
Glu Ile Asn Val Arg Arg Ala Ser Glu Leu Leu Asn Met Ala Lys Arg		
1075	1080	1085
Leu Ser Ala Ser Thr Leu Arg Leu Pro Ala Ser Leu Val Phe Asp Thr		
1090	1095	1100
Val Thr Ala Leu Gln His Leu Arg Ala Arg Val Gly Asp Ala Asp Gln		
1105	1110	1115
Ala Ala Val Arg Val Val Gly Ala		
1125		

<210> 39
<211> 1224
<212> PRT
<213> Artificial Sequence

<220>
<223> Alignment of the EryA SU

<400> 39
Ala Asp Glu Ser Glu Ile Ile Gly Ile Gly Phe Gly Ile Gly Ser Glu
1 5 10 15
Gln Leu Arg Val Leu Ala Glu Gly Ala Asn Leu Thr Thr Gly Phe Ala
20 25 30
Asp Ile Gly Arg Leu Tyr His Pro Asp Pro Asp Asn Pro Gly Thr Ser
35 40 45
Tyr Val Asp Lys Gly Pro Leu Thr Asp Ala Asp Pro Gly Ile Thr Leu
50 55 60
Met Leu Met Thr Ala Ala Val Arg Ile Asp Asp Ala Arg Gly Thr Asp
65 70 75 80
Val Met Asn Gly Gln Ser Met Gln Leu Leu Ala Gly Glu Ala Glu Arg
85 90 95
Val Asp Gln Gly Ile Asn Ser Ala Ser Leu Ile Ala Thr Phe Trp Ala
100 105 110
Leu Thr Ser Val Gly Ile Ile Met Gln Ala Arg Gly Glu Cys Ser Leu
115 120 125
Leu Ala Val Thr Ser Asp Tyr Thr Phe Val Asp Ser Thr Gln Arg Gly
130 135 140
Ala Ser Cys Ala Ser Ala Arg Asp Ala Leu Ser Val Ala Ala Leu Val
145 150 155 160
Glu Pro Arg Ala Asn His Gln Ala Val Leu Arg Ser Val Gln Ala Asn
165 170 175
Pro Ser Glu Arg Gln Leu Ala Ala Ser Val Pro Ala Ala Val Asp Val
180 185 190
Glu Ile Ala Gly Ile Ala Thr Gln Asp Asp Arg Leu Arg Leu Thr Ile
195 200 205
Thr Ala Ala Ile Val Val Ala Met Arg His Met Leu Arg Ser His Ala
210 215 220
Asp Leu Ser Pro His Ile Asp Glu Ser Ala Val Glu Val Ile Arg Glu
225 230 235 240
Glu Val Pro Pro Ala Gly Glu Arg Pro Gly Ser Val Val Val Glu Ala
245 250 255
Ala Glu Gln Glu Ala Ala Arg Thr Glu Arg Gly Pro Leu Phe Val Leu
260 265 270
Gly Arg Ser Glu Ala Val Val Ala Arg Ala Leu Ala Glu His Leu Arg
275 280 285
Asp Thr Pro Glu Leu Gly Leu Thr Asp Ala Ala Trp Thr Leu Thr Gly
290 295 300
Ala Arg Phe Asp Val Ala Val Gly Asp Asp Arg Ala Gly Val Cys Ala
305 310 315 320
Glu Asp Ala Leu Glu Arg Pro Ser Ala Asp Ala Val Ala Pro Val Thr
325 330 335
Ser Ala Pro Arg Lys Pro Val Leu Val Ala Val Ala Arg Asp Glu Ser
340 345 350
Ser Glu Glu Ser Met Ser Arg Ala Glu Ala Leu Ser Pro His Thr Asp
355 360 365
Trp Lys Leu Leu Asp Val Val Arg Gly Asp Gly Gly Pro Asp Pro His
370 375 380
Glu Asp Ile Val Leu Ser Ile Met Val Glu Leu Arg Ala His Val Thr
385 390 395 400
Ala Val Gln Ile His Ala Ala Leu Ser Leu Glu Ala Ala Ala Lys Val
405 410 415

Val Ala Leu Arg Ser Gln Val Leu Arg Glu Leu Asp Asp Gln Gly Gly
 420 425 430
 Val Ser Val Gly Ala Ser Arg Asp Glu Leu Glu Thr Val Leu Ala Arg
 435 440 445
 Trp Asp Gly Arg Val Ala Val Ala Gly Gly Thr Ser Val Val Ala Pro
 450 455 460
 Thr Ala Glu Leu Asp Glu Phe Phe Ala Glu Ala Glu Ala Arg Glu Met
 465 470 475 480
 Lys Pro Arg Arg Ile Ala Arg Tyr Ser Ser Pro Glu Val Ala Arg Ile
 485 490 495
 Glu Asp Arg Ile Ala Ala Glu Leu Gly Thr Ile Thr Ala Val Arg Gly
 500 505 510
 Ser Val Pro Leu His Thr Val Thr Gly Glu Val Ile Asp Thr Ser Ala
 515 520 525
 Met Asp Ala Ser Tyr Arg Asn Ile Arg Pro Leu Glu Gln Val Arg Gly
 530 535 540
 Leu Val Glu Gln Phe Asp Thr Val Val Pro Val Leu Leu Met Ala Val
 545 550 555 560
 Glu Glu Thr Ala Glu His Ala Gly Ala Glu Val Thr Cys Val Pro Thr
 565 570 575
 Arg Glu Gln Ser Gly Pro His Glu Phe Leu Arg Asn Leu Leu Arg His
 580 585 590
 Val His Gly Ala Asp Leu Arg Pro Ala Val Ala Gly Gly Arg Pro Ala
 595 600 605
 Glu Thr Glu His Gln Phe Pro Arg Pro His Arg Pro Ala Asp Val Ser
 610 615 620
 Ala Leu Tyr Gly Leu Ala Glu Gln Gly Glu Tyr Gly Pro Ser Phe Gln
 625 630 635 640
 Ala Leu Arg Ala Ala Arg Lys Asp Asp Ser Val Tyr Ala Glu Val Ser
 645 650 655
 Ile Ala Ala Asp Glu Glu Gly Tyr Ala Phe His Pro Val Leu Asp Ala
 660 665 670
 Val Ala Gln Thr Leu Ser Leu Gly Ala Leu Gly Glu Pro Gly Gly Gly
 675 680 685
 Lys Leu Pro Phe Ala Trp Asn Thr Val Thr Leu His Ala Ser Ala Thr
 690 695 700
 Ser Val Arg Val Val Ala Thr Pro Ala Gly Ala Asp Ala Met Ala Leu
 705 710 715 720
 Arg Val Thr Asp Pro Ala Gly His Leu Val Ala Thr Asp Leu Val Val
 725 730 735
 Arg Ser Thr Gly Glu Lys Trp Glu Gln Pro Glu Pro Arg Gly Gly Glu
 740 745 750
 Gly Glu Leu His Ala Asp Trp Gly Arg Leu Ala Glu Pro Gly Ser Thr
 755 760 765
 Gly Arg Val Val Ala Ala Asp Ala Ser Asp Leu Asp Ala Val Leu Arg
 770 775 780
 Ser Gly Glu Pro Glu Pro Asp Ala Val Leu Val Arg Tyr Glu Pro Glu
 785 790 795 800
 Gly Asp Asp Pro Arg Ala Ala Ala Arg His Gly Val Leu Trp Ala Ala
 805 810 815
 Ala Leu Val Arg Arg Trp Leu Glu Gln Glu Leu Pro Gly Ala Thr
 820 825 830
 Leu Val Ile Ala Ser Gly Thr Val Ser Asp Asp Asp Ser Val Pro Glu
 835 840 845
 Pro Gly Ala Ala Ala Met Trp Val Ile Arg Cys Ala Gln Ala Ser Pro
 850 855 860
 Asp Arg Phe Val Leu Leu Thr Asp Ala Glu Pro Gly Met Leu Pro Val
 865 870 875 880
 Pro Asp Asn Pro Gln Leu Leu Gly Asp Asp Val Phe Val Pro Leu Ser
 885 890 895
 Pro Leu Ala Pro Ser Ala Thr Gln Pro Ala Pro Val Asp Asp Val Ile
 900 905 910

Gly Thr Gly Thr Leu Arg Leu Leu Ala His Val Thr His Glu Val Arg
 915 920 925
 His Leu Val Ser Arg Arg Gly Ala Asp Ala Pro Gly Ser Asp Glu Arg
 930 935 940
 Ala Glu Ile Glu Asp Ile Ala Ser Ala Glu Ile Ala Cys Thr Ala Asp
 945 950 955 960
 Arg Asp Ala Leu Ser Ala Leu Leu Asp Gly Leu Pro Arg Pro Leu Thr
 965 970 975
 Gly Val Val Ala Ala Gly Val Leu Ala Asp Gly Leu Val Thr Ser Ile
 980 985 990
 Asp Glu Pro Ala Val Glu Gln Val Leu Arg Ala Val Asp Ala Ala Trp
 995 1000 1005
 Asn His Leu Thr Ala Asn Thr Gly Leu Ser Phe His Val Leu Phe Ala
 1010 1015 1020
 Ser Val Leu Ala Gly Pro Gly Gln Gly Val Ala Ala Ala Asn Glu Ser
 1025 1030 1035 1040
 Asn Ala Leu Ala Leu Arg Thr Arg Leu Pro Ala Lys Ala Leu Gly Gly
 1045 1050 1055
 Leu Gln Ala Ser Glu Met Thr Ser Gly Leu Gly Asp Arg Ile Ala Arg
 1060 1065 1070
 Thr Val Ala Ala Leu Pro Thr Glu Arg Leu Ala Leu Phe Asp Ser Ala
 1075 1080 1085
 Arg Arg Gly Gly Glu Val Val Phe Pro Leu Ser Ile Asn Arg Ser Ala
 1090 1095 1100
 Leu Arg Arg Glu Phe Val Pro Glu Val Leu Arg Gly Met Val Arg Ala
 1105 1110 1115 1120
 Lys Leu Arg Ala Ala Gly Gln Ala Glu Ala Ala Gly Pro Asn Val Val
 1125 1130 1135
 Asp Arg Leu Gly Arg Ser Glu Ser Asp Gln Val Ala Gly Ala Glu Leu
 1140 1145 1150
 Val Arg Ser His Ala Ala Val Ser Tyr Gly Ser Ala Asp Gln Leu Pro
 1155 1160 1165
 Glu Arg Lys Ala Lys Asp Phe Leu Ala Val Glu Asn Arg Leu Gly Thr
 1170 1175 1180
 Ala Thr Val Arg Leu Pro Ser Thr Leu Val Phe Asp Thr Pro Leu Ala
 1185 1190 1195 1200
 Val Glu His Leu Arg Asp Arg Phe Ala Ala Ser Pro Ala Val Asp Ile
 1205 1210 1215
 Gly Asp Arg Leu Asp Glu Leu Glu
 1220

<210> 40
 <211> 1118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Alignment of the EryA SU

<400> 40
 His Arg Ala Gly Glu Ile Ile Gly Met Ala Phe Asp Val Asp Ser Glu
 1 5 10 15
 Ser Phe Glu Phe Val Ser Gly Gly Asp Ala Ile Ala Glu Ala Ala
 20 25 30
 Glu Pro Asp Pro Asp Ala Arg Leu Gly Met Leu Ala Ala Gly Asp Ala
 35 40 45
 Gly Ile Ser Leu Met Ile Met Ile Ser Ala Leu Arg His Asp Val Ser
 50 55 60
 Arg Gly Ser Ala Ile Val Gly Thr Val Asp Gly Pro Arg Pro Asp Glu
 65 70 75 80
 Ala Pro Asp Glu Val Leu Val Gly Thr Thr Ala Ser Ser Ala Val Ala

85	90	95
Cys Leu Leu Ala Met Thr Gly Thr	Ala Leu Ile Met Glu Ser Arg Asp	
100	105	110
Glu Cys Gly Leu Ile Ala Val Thr Ser Ser Gly Ala Phe Thr Glu Arg		
115	120	125
Ser Gln Gly Gly Ala Ala Cys Pro Ser Lys Ala Asp Gly Leu Ala Ala		
130	135	140
Gly Val Leu Val Gln Arg Ala Arg Glu Arg Pro Ala Val Leu Arg Ser		
145	150	155
Val Gln Thr Ser Pro Ala Gln Arg Arg Leu Glu Asn Ala Val Arg Ala		
165	170	175
Gly Val Asp Tyr Arg Ile Val His Leu Ser Thr Ala Glu Asp Pro Asp		
180	185	190
Asp Leu Trp Ile Ser Ile Thr Val Ala Met Ala Val Ala Leu Arg His		
195	200	205
Glu Met Arg Thr His Phe Asp Pro Ser Pro Gln Ile Glu Asp Leu Ala		
210	215	220
Val Ser Val Val Ser Gln Ala Arg Ser Pro Ala Gly Glu Arg Pro Gly		
225	230	235
Ser Ile Val Val Glu Ala Glu Ala Asp Glu Pro Glu Pro Ala Pro Asp		
245	250	255
Ser Gly Pro Val Leu Val Leu Gly Arg Asp Glu Gln Ala Met Arg Gly		
260	265	270
Arg Leu Ala Asp His Leu Ala Arg Glu Pro Arg Asn Ser Leu Arg Asp		
275	280	285
Thr Gly Phe Thr Leu Thr Arg Ser Ala Trp Glu His Val Val Val Gly		
290	295	300
Asp Arg Asp Asp Ala Leu Ala Gly Arg Ala Val Asp Arg Ile Ala Asp		
305	310	315
Arg Thr Ala Thr Gly Gln Ala Arg Thr Arg Arg Gly Val Ala Met Val		
325	330	335
Ala Gln Ala Arg Asp Arg Glu Ser Gln Asp Ser Ile Arg Asp Glu Arg		
340	345	350
Ala Leu Ala Pro His Val Asp Trp Ser Leu Thr Asp Leu Leu Ser Gly		
355	360	365
Ala Arg Pro Leu Asp Asp Val Ala Leu Ala Val Met Val Ala Leu Arg		
370	375	380
Ser His Val Glu Ala Val Gln Ile His Ala Ala Leu Thr Leu Glu Asp		
385	390	395
Ala Ala Lys Leu Val Ala Val Arg Ser Arg Val Leu Ala Arg Leu Gly		
405	410	415
Gly Gln Gly Ala Ser Phe Gly Leu Gly Thr Glu Gln Ala Ala Glu		
420	425	430
Arg Ile Gly Arg Phe Ala Gly Ala Leu Ser Ile Ser Gly Arg Ser Val		
435	440	445
Val Val Ala Glu Ser Gly Pro Leu Asp Glu Leu Ile Ala Glu Cys Glu		
450	455	460
Ala Glu Gly Ile Thr Ala Arg Arg Ile Pro Asp Tyr Ser Ser Pro Gln		
465	470	475
Val Glu Ser Ile Arg Glu Glu Leu Leu Thr Glu Leu Ala Gly Ile Ser		
485	490	495
Pro Val Ser Ala Asp Val Ala Leu Tyr Thr Thr Gly Gln Pro Ile		
500	505	510
Asp Thr Ala Thr Met Asp Thr Ala Tyr Ala Asn Leu Glu Gln Arg Gln		
515	520	525
Asp Thr Arg Gln Leu Ala Glu Ala Phe Asp Ala Val Val Pro Val Leu		
530	535	540
Thr Val Gly Ile Glu Ala Thr Leu Asp Ser Ala Leu Pro Ala Asp Ala		
545	550	555
Gly Ala Cys Val Val Gly Thr Arg Asp Arg Gly Gly Leu Ala Asp Phe		
565	570	575
His Thr Ala Leu Gly Glu Tyr Ala Gln Glu Val Asp Trp Ser Pro Ala		

580	585	590
Phe Ala Asp Ala Arg Pro Val Glu Val Gln Arg Gln Tyr		Leu Pro Ile
595	600	605
Pro Thr Gly Gly Arg Ala Arg Glu Asp Asp Asp Trp Arg		Gln Val Val
610	615	620
Arg Glu Ala Glu Trp Glu Ser Ala Ser Leu Ala Gly Arg		Val Leu Val
625	630	635
Thr Gly Pro Gly Val Pro Ser Glu Leu Ser Asp Ala Ile		Arg Ser Gly
645	650	655
Leu Glu Gln Ser Ala Thr Val Leu Thr Cys Asp Val Glu		Ser Arg Ser
660	665	670
Thr Ile Gly Thr Ala Leu Glu Ala Ala Asp Thr Asp Ala		Leu Ser Thr
675	680	685
Val Leu Leu Ser Arg Asp Gly Glu Ala Val Asp Pro Ser		Leu Asp Ala
690	695	700
Leu Ala Val Gln Ala Leu Gly Ala Ala Gly Val Glu Ala		Pro Leu Trp
705	710	715
Val Leu Arg Asn Gln Val Ala Asp Gly Glu Leu Val Asp		Pro Ala Gln
725	730	735
Ala Met Val Gly Leu Gly Arg Val Val Gly Ile Gln Pro		Gly Arg Trp
740	745	750
Gly Gly Leu Val Leu Val Asp Ala Asp Ala Ala Ser Ile		Arg Ser Leu
755	760	765
Ala Val Leu Ala Asp Pro Arg Gly Glu Glu Gln Val Ile		Ala Asp Gly
770	775	780
Ile Lys Val Ala Leu Val Pro Ala Pro Ala Arg Ala Ala		Arg Thr Arg
785	790	795
Trp Ser Arg Val Val Gly Thr Gly Gly Ile Ala His Val		Ala Trp Ala
805	810	815
Arg Ser Ala Glu His Val Leu Gly Arg Arg Gly Ala Asp		Ala Pro Gly
820	825	830
Ala Ser Glu Arg Glu Glu Leu Thr Ala Leu Thr Gly Val		Thr Ile Ala
835	840	845
Cys Val Ala Asp Arg Ala Arg Leu Glu Ala Val Leu Ala		Ala Glu Arg
850	855	860
Ala Glu Gly Arg Thr Val Ser Ala Val Met Ala Ala Gly		Val Ser Thr
865	870	875
Ser Thr Pro Leu Asp Asp Leu Thr Glu Ala Glu Phe Thr		Glu Ile Ala
885	890	895
Asp Val Val Arg Gly Thr Val Asn Asp Leu Cys Pro Asp		Leu Asp Ala
900	905	910
His Val Leu Phe Asn Gly Val Trp Gly Ser Pro Gly Leu		Ala Ser Ala
915	920	925
Ala Ala Asn Ala Phe Asp Gly Phe Arg Arg Arg Ser		Glu Ala Pro Val
930	935	940
Thr Ser Ile Ala Gly Leu Gly Gln Asn Met Ala Gly Asp		Glu Gly Gly
945	950	955
Glu Tyr Leu Arg Ser Gln Leu Arg Ala Met Asp Pro Asp		Arg Val Glu
965	970	975
Glu Leu His Ile Thr Asp His Gly Gln Thr Ser Val Ser		Val Val Asp
980	985	990
Met Asp Arg Arg Arg Phe Val Glu Leu Phe Thr Ala Arg		His Arg Pro
995	1000	1005
Leu Phe Asp Glu Ile Ala Gly Ala Arg Ala Glu Ala Arg		Gln Ser Glu
1010	1015	1020
Glu Gly Pro Ala Leu Ala Gln Arg Leu Ala Leu Ser Thr		Ala Glu Arg
1025	1030	1035
Arg Glu His Ala His Leu Ile Arg Ala Glu Val Ala Val		Leu His Gly
1045	1050	1055
Asp Asp Ala Ala Ile Asp Arg Asp Arg Ala Arg Asp Phe		Met Thr Val
1060	1065	1070
Asp Asn Arg Leu Ala Ala Val Thr Val Arg Glu Ala Ala		Thr Val Val

1075	1080	1085
Phe Asp Thr Ile Thr Arg Leu Asp His Tyr Leu Glu Arg Val Gly Ala		
1090	1095	1100
Ala Glu Ala Glu Gln Ala Pro Ala Leu Val Arg Glu Val Pro		
1105	1110	1115

<210> 41
<211> 1099
<212> PRT
<213> Artificial Sequence

<220>
<223> Alignment of the EryA SU

<400> 41		
Lys Asp Ala Asp Asp Ile Ile Gly Met Ala Phe Gly Val His Asn Gly		
1 5 10 15		
Glu Leu Glu Phe Ile Val Gly Arg Gly Asp Ala Val Thr Glu Met Thr		
20 25 30		
Asp Leu Asp Ala Leu Phe Asp Pro Asp Pro Gln Arg His Gly Thr Ser		
35 40 45		
Tyr Ser Arg His Ala Phe Leu Asp Gly Ala Asp Ala Ala Ile Ser Leu		
50 55 60		
Met Gln Val Thr Thr Leu Phe Asn Ile Asp His Ser Arg Gly Ser Asp		
65 70 75 80		
Leu Ala Ala Tyr Gln Gly Gly Gln Asp Ala Val Val Pro Glu Asp Ser		
85 90 95		
Glu Leu Leu Thr Asn Ser Ser Ala Val Val Ala Val Leu Leu Ala Val		
100 105 110		
Thr Ser Val Ala Leu Ser Cys Gly Ser Asp Gly Asp Cys Gly Leu Val		
115 120 125		
Ala Val Ser Ala Gly Glu Val Phe Thr Glu Ser Arg Gln Gly Gly Ala		
130 135 140		
Val Cys Ala Ser Ala Glu Asp Gly Phe Ala Val Ala Val Val Leu Gln		
145 150 155 160		
Arg Asp Arg Ala Arg Gln Gly Val Val Ala Ser Leu Gln Ala Ser Val		
165 170 175		
Ala Gln Arg Lys Trp Ala Arg Ala Ile Thr Gly Ala Val Ala Val Arg		
180 185 190		
Val Ala Ser Leu Ala Thr Lys Ser Gly Ser Ser Gly Val Leu Leu Ser		
195 200 205		
Ile Ala Val Ala Ile Val Val Gly Leu Asn Arg Leu Val Pro Met Cys		
210 215 220		
Arg Gly Arg Ser Pro Leu Ile Glu Ser Ser Gly Val Glu Leu Ala Glu		
225 230 235 240		
Ala Val Ser Pro Pro Ala Ala Asp Gly Val Gly Ala Val Val Ile		
245 250 255		
Ala Pro Glu Pro Glu Pro Leu Pro Glu Pro Gly Pro Val Gly Val Leu		
260 265 270		
Ala Ala Ala Asn Ser Val Val Leu Leu Ala Arg Thr Glu Thr Ala Leu		
275 280 285		
Ala Arg Leu Leu Glu Ser Ala Val Asp Asp Ser Val Pro Leu Thr Ala		
290 295 300		
Leu Ala Ser Ala Leu Thr Gly Ala His Leu Pro Arg Ala Leu Ile Ala		
305 310 315 320		
Gly Asp His Glu Gln Leu Arg Gly Gln Arg Ala Val Glu Val Ala Ala		
325 330 335		
Pro Gly Ala Thr Thr Gly Thr Ala Ser Ala Gly Gly Val Val Phe Val		
340 345 350		
Ala Glu Ala Arg Gly Ser Val Pro Glu Ser Ile Ala Glu Asp Ala Val		
355 360 365		

Leu Ser Glu Val Ala Gly Phe Ser Ala Ser Glu Val Leu Glu Gln Arg
 370 375 380
 Pro Asp Ala Pro Ser Leu Glu Asp Val Val Leu Ser Val Met Val Arg
 385 390 395 400
 Leu Gly Ala Cys Val Ser Ser Ile Gln Ile Val Ala Val Leu Ser Leu
 405 410 415
 Glu Asp Gly Val Arg Val Val Ala Leu Arg Ala Lys Ala Leu Arg Ala
 420 425 430
 Leu Ala Gly Arg Gly Val Ser Leu Ala Ala Pro Gly Glu Arg Ala
 435 440 445
 Arg Ala Leu Ile Ala Pro Trp Glu Asp Arg Ile Ser Val Ala Ser Ser
 450 455 460
 Ser Val Val Val Ser Asp Pro Glu Ala Leu Ala Glu Leu Val Ala Arg
 465 470 475 480
 Cys Glu Asp Glu Gly Val Arg Ala Lys Thr Leu Pro Asp Tyr Ser Ser
 485 490 495
 Arg His Val Glu Glu Ile Arg Glu Thr Ile Leu Ala Asp Leu Asp Gly
 500 505 510
 Ile Ser Ala Arg Arg Ala Ala Ile Pro Leu Tyr Thr Leu His Gly Glu
 515 520 525
 Arg Arg Asp Gly Ala Asp Met Gly Pro Arg Tyr Asp Asn Leu Ser Gln
 530 535 540
 Arg Asp Glu Val Ser Ala Ala Val Ala Asp His Ala Thr Val Met Pro
 545 550 555 560
 Val Ile Thr Ala Ala Val Gln Glu Ile Ala Ala Asp Ala Val Ala Ile
 565 570 575
 Gly Ser His Asp Thr Ala Glu Glu His Ile Ile Ala Glu Leu Ala Arg
 580 585 590
 His Val His Ala Val Asp Trp Arg Asx Val Phe Pro Ala Ala Pro Pro
 595 600 605
 Val Ala Asn Glu Pro Gln Tyr Leu Ala Pro Glu Val Ser Gln Leu Ala
 610 615 620
 Asp Ser Arg Arg Val Asp Arg Pro Leu Ala Thr Thr Pro Val Asp Leu
 625 630 635 640
 Glu Gly Gly Phe Val His Gly Ser Ala Pro Glu Ser Leu Thr Ser Ala
 645 650 655
 Val Glu Lys Ala Gly Arg Val Val Pro Val Ala Ser Ala Asp Arg Glu
 660 665 670
 Ala Ser Ala Ala Leu Arg Glu Val Pro Gly Glu Val Ala Gly Leu Val
 675 680 685
 His Thr Gly Ala Ala Thr His Leu Ala His Gln Ser Leu Gly Glu Ala
 690 695 700
 Gly Val Arg Ala Pro Leu Trp Leu Val Ser Arg Ala Leu Gly Glu Ser
 705 710 715 720
 Glu Pro Val Asp Pro Glu Gln Ala Met Val Trp Leu Gly Arg Val Met
 725 730 735
 Gly Leu Thr Pro Glu Arg Trp Gly Gly Leu Val Leu Pro Ala Glu Pro
 740 745 750
 Ala Pro Gly Asp Gly Glu Ala Phe Val Cys Leu Gly Ala Asp Gly His
 755 760 765
 Glu Asp Gln Val Ile Asp His Ala Arg Tyr Gly Arg Leu Val Arg Ala
 770 775 780
 Pro Leu Gly Thr Arg Glu Ser Ser Trp Glu Ala Ala Val Gly Thr Gly
 785 790 795 800
 Ala Leu Gly His Val Ala His Ala Arg Cys Val Glu Asp Val Val Ser
 805 810 815
 Arg Arg Gly Val Asp Ala Pro Gly Ala Ala Glu Glu Ala Glu Leu Val
 820 825 830
 Ala Ile Ala Lys Thr Thr Ile Thr Cys Val Ala Asp Arg Glu Gln Leu
 835 840 845
 Ser Lys Leu Leu Glu Glu Leu Arg Gly Gln Gly Arg Pro Val Arg Thr
 850 855 860

Val Val Thr Ala Gly Val Pro Glu Ser Arg Pro Leu His Glu Ile Gly
865 870 875 880
Glu Leu Glu Ser Val Cys Ala Ala Val Thr Gly Ala Arg Leu Asp Leu
885 890 895
Cys Pro Asp Ala Glu Thr His Val Leu Phe Gly Gly Val Trp Gly Ser
900 905 910
Ala Asn Leu Gly Ala Ser Ala Ala Asn Ala Tyr Asp Ala Leu His Arg
915 920 925
Arg Ala Glu Arg Ala Ala Thr Ser Val Ala Gly Ala Gly Glu Gly Met
930 935 940
Ala Thr Gly Asp Leu Glu Gly Leu Thr Arg Arg Leu Arg Pro Met Ala
945 950 955 960
Pro Glu Arg Ile Arg Ala Leu His Gln Ala Asp Asn Gly Asp Thr Cys
965 970 975
Val Ser Ile Ala Asp Val Asp Trp Glu Ala Phe Ala Val Gly Phe Thr
980 985 990
Ala Arg Pro Arg Pro Leu Leu Asp Glu Leu Val Thr Pro Ala Val Gly
995 1000 1005
Ala Val Pro Ala Val Gln Ala Pro Ala Arg Glu Met Thr Ser Gln Glu
1010 1015 1020
Leu Glu Phe Thr His Ser His Val Ala Ile Leu His Ser Ser Pro Asp
1025 1030 1035 1040
Ala Val Gly Gln Asp Gln Pro Thr Glu Phe Leu Thr Val Gly Asn Gln
1045 1050 1055
Leu Gln Gln Ala Thr Leu Ala Leu Pro Ala Thr Leu Val Phe Glu Thr
1060 1065 1070
Val Arg Arg Leu Asp His Ile Gly Gln Gln Asp Ser Gly Thr Pro Ala
1075 1080 1085
Arg Glu Ala Ser Ser Ala Leu Arg Asp Gly Tyr
1090 1095